

SEQUENCE LISTING

<110> Miller, Duane D.
 Tigyi, Gabor
 Dalton, James T.
 Sardar, Vineet M.
 Elrod, Don B.
 Xu, Huiping
 Baker, Daniel L.
 Wang, Dean
 Liliom, Karoly
 Fischer, David J.
 Virag, Tamas
 Nusser, Nora

<120> LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
 USE

<130> 20609/181

<140>

<141>

<150> 60/190,370

<151> 2000-03-17

<160> 26

<170> PatentIn Ver. 2.1

<210> 1

<211> 1095

<212> DNA

<213> Homo sapiens

<400> 1

```
atggctgcc tctctacttc catccctgta atttcacagc cccagttcac agccatgaat 60
gaaccacagt gcttctacaa cgagtcatt gccttctttt ataaccgaag tggaaagcat 120
cttgccacag aatggaacac agtcagcaag ctggtgatgg gacttggaat cactgtttgt 180
atcttcatca tgttggccaa cctattggtc atggtggcaa tctatgtcaa ccgccgttc 240
cattttccta ttattacct aatggcta atctggtgctg cagacttctt tgctgggttg 300
gcctacttct atctcatgtt caacacagga cccaatactc ggagactgac tgtagcaca 360
tggtctctgc gtcagggcct cattgacacc agcctgacgg catctgtggc caacttactg 420
gctattgcaa tcgagaggca cattacggtt ttccgcatgc agctccacac acggatgagc 480
aaccggcggg tagtggtggt cattgtggtc atctggacta tggccatcgt tatgggtgct 540
ataccagtg tgggctggaa ctgtatctgt gatattgaaa attgttcaa catggcacc 600
ctctacagt actcttactt agtcttctgg gccattttca acttggtgac ctttgtggta 660
atggtggttc tctatgctca catctttggc tatgttcgcc agaggactat gagaatgtct 720
```

```

cggcatagtt ctggaccccg gcggaatcgg gataccatga tgagtcttct gaagactgtg 780
gtcattgtgc ttggggcctt tatcatctgc tggactcctg gattgggttt gttacttcta 840
gacgtgtgct gtccacagtg cgacgtgctg gcctatgaga aattcttcct tctccttgct 900
gaattcaact ctgcatgaa ccccatcatt tactcctacc gcgacaaaga aatgagcgcc 960
acctttaggc agatcctctg ctgccagcgc agtgagaacc ccaccggccc cacagaaagc 1020
tcagaccgct cggcttcctc cctcaaccac accatcttgg ctggagttca cagcaatgac 1080
cactctgtgg tttag 1095

```

```

<210> 2
<211> 364
<212> PRT
<213> Homo sapiens

```

```

<400> 2
Met Ala Ala Ile Ser Thr Ser Ile Pro Val Ile Ser Gln Pro Gln Phe
  1             5             10            15

Thr Ala Met Asn Glu Pro Gln Cys Phe Tyr Asn Glu Ser Ile Ala Phe
      20             25            30

Phe Tyr Asn Arg Ser Gly Lys His Leu Ala Thr Glu Trp Asn Thr Val
      35             40            45

Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Ile Phe Ile Met
      50             55            60

Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
      65             70            75            80

His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe
      85             90            95

Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn
      100            105            110

Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile
      115            120            125

Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile
      130            135            140

Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser
      145            150            155            160

Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile
      165            170            175

```

Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile
 180 185 190

Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val
 195 200 205

Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu
 210 215 220

Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser
 225 230 235 240

Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu
 245 250 255

Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr
 260 265 270

Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp
 275 280 285

Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser
 290 295 300

Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala
 305 310 315 320

Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly
 325 330 335

Pro Thr Glu Ser Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile
 340 345 350

Leu Ala Gly Val His Ser Asn Asp His Ser Val Val
 355 360

<210> 3

<211> 1056

<212> DNA

<213> Homo sapiens

<400> 3

atgggtcatca tgggccagtg ctactacaac gagaccatcg gcttctttota taacaacagt 60
 ggcaaagagc tcagctccca ctggcgcccc aaggatgtgg tcgtggtggc actggggctg 120
 accgtcagcg tgctggtgct gctgaccaat ctgctggtca tagcagccat cgcctccaac 180
 cgccgcttcc accagcccat ctactacctg ctcggaatc tggcgcgggc tgacctcttc 240
 gcgggcgtgg cctacctctt cctcatgttc cacactggtc cccgcacagc cgcactttca 300

```

cttgaggggt ggttcctgcg gcagggcttg ctggacacaa gcctcactgc gtcgggtggcc 360
acactgctgg ccatcgccgt ggagcggcac cgcagtgtga tggccgtgca gctgcacagc 420
cgccctgcccc gtggccgcgt ggtcatgctc attgtgggcg tgtgggtggc tgccctgggc 480
ctggggctgc tgctgcccc ctccctggcac tgccctctgt ccctggaccg ctgctcacgc 540
atggcacccc tgctcagccg ctccctatttg gccgtctggg ctctgtcgag cctgcttgtc 600
ttcctgctca tggtggtgt gtacacccgc attttcttct acgtgcggcg gcgagtgcag 660
cgcatggcag agcatgtcag ctgccacccc cgctaccgag agaccacgct cagcctggtc 720
aagactgttg tcatcatcct gggggcggtt gtggtctgct ggacaccagg ccaggtggta 780
ctgctcctgg atggttttag ctgtgagtcc tgcaatgtcc tggctgtaga aaagtacttc 840
ctactgttgg ccgaggccaa ctcaactggc aatgctgctg tgtactcttg ccgagatgct 900
gagatgcgcc gcaccttccg ccgccttctc tgctgcgcgt gcctccgcc gtccacccgc 960
gagtcgtgcc actatacatc ctctgccag ggaggtgcc gcactcgcac catgcttccc 1020
gagaacggcc acccactgat ggactccacc ctttag 1056

```

<210> 4

<211> 351

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Val Ile Met Gly Gln Cys Tyr Tyr Asn Glu Thr Ile Gly Phe Phe
  1             5             10             15

```

```

Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp
      20             25             30

```

```

Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
      35             40             45

```

```

Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
      50             55             60

```

```

Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Asp Leu Phe
      65             70             75             80

```

```

Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
      85             90             95

```

```

Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
      100            105            110

```

```

Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
      115            120            125

```

```

Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
      130            135            140

```

Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
145 150 155 160

Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
165 170 175

Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
180 185 190

Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
195 200 205

Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
210 215 220

His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
225 230 235 240

Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
245 250 255

Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
260 265 270

Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
275 280 285

Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg
290 295 300

Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
305 310 315 320

Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
325 330 335

Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Asp Ser Thr Leu
340 345 350

<210> 5

<211> 1062

<212> DNA

<213> Homo sapiens

<400> 5

atgaatgagt gtcactatga caagcacatg gacttttttt ataataggag caacactgat 60
actgtcgatg actggacagg aacaaagctt gtgattgttt tgtgtgttgg gacgtttttc 120

```

tgccctgttta tttttttttc taattctctg gtcacgcgg cagtgatcaa aaacagaaaa 180
tttcatttcc ctttctacta cctgttggt aatttagctg ctgccgattt cttcgctgga 240
attgcctatg tattcctgat gtttaacaca ggcccagttt caaaaacttt gactgtcaac 300
cgctggtttc tccgtcaggg gcttctggac agtagcttga ctgcttccct caccaacttg 360
ctgggttatcg ccgtggagag gcacatgtca atcatgagga tgcgggtcca tagcaacctg 420
accaaaaaga gggtgacact gctcattttg cttgtctggg ccatcgccat ttttatgggg 480
gcgggtcccca cactgggctg gaattgcctc tgcaacatct ctgcctgctc ttccctggcc 540
cccatttaca gcaggagtta cttgttttc tggacagtgt ccaacctcat ggccttctc 600
atcatgggtg tgggtgtacct gcggatctac gtgtacgtca agaggaaaac caacgtcttg 660
tctccgcata caagtgggtc catcagcgc cggaggacac ccatgaagct aatgaagacg 720
gtgatgactg tcttaggggc gtttgtggta tgctggaccc cgggcctggg ggttctgctc 780
ctcgacggcc tgaactgcag gcagtgtggc gtgcagcatg tgaaaagggt gttcctgctg 840
ctggcgctgc tcaactccgt cgtgaacccc atcatctact cctacaagga cgaggacatg 900
tatggcacca tgaagaagat gatctgctgc ttctctcagg agaaccaga gaggcgtccc 960
tctcgcatcc cctccacagt cctcagcagg agtgacacag gcagccagta catagaggat 1020
agtattagcc aaggtgcagt ctgcaataaa agcacttct aa 1062

```

<210> 6

<211> 353

<212> PRT

<213> Homo sapiens

<400> 6

```

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
  1                      5                      10                      15

```

```

Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
          20                      25                      30

```

```

Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
          35                      40                      45

```

```

Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
          50                      55                      60

```

```

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
          65                      70                      75                      80

```

```

Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
          85                      90                      95

```

```

Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
          100                      105                      110

```

```

Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
          115                      120                      125

```

Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
 130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
 145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
 165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr
 180 185 190

Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg
 195 200 205

Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
 210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr
 225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
 245 250 255

Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
 260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
 275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met
 290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro
 305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln
 325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr
 340 345 350

Ser

<210> 7

<211> 1260

<212> DNA
 <213> Homo sapiens

<400> 7

```

atggtcttct cggcagtgtt gactgogttc cataccggga catccaacac aacatttgtc 60
gtgtatgaaa acacctacat gaatattaca ctccctccac cattccagca tcctgacctc 120
agtccattgc ttagatatag ttttgaaacc atggctccca ctggtttgag ttccttgacc 180
gtgaatagta cagctgtgcc cacaacacca gcagcattta agagcctaaa cttgcctctt 240
cagatcacc cttctgctat aatgatattc attctgtttg tgtcttttct tgggaacttg 300
gttgtttgcc tcatggttta ccaaaaagct gccatgaggt ctgcaattaa catcctcctt 360
gccagcctag cttttgcaga catgttgctt gcagtgtga acatgccctt tgccctggta 420
actattctta ctaccgatg gatTTTTggg aaattcttct gtagggatct tgctatgttt 480
ttctggttat ttgtgataga aggagtagcc atcctgctca tcattagcat agatagggtt 540
cttattatag tccagaggca ggataagcta aaccatata gagctaaggt tctgattgca 600
gtttcttggg caacttcctt ttgtgtagct tttcctttag ccgtaggaaa ccccgacctg 660
cagatacctt cccgagctcc ccagtgtgtg tttgggtaca caaccaatcc aggctaccag 720
gcttatgtga ttttgatttc tctcatttct ttcttcatac ccttcctggg aatactgtac 780
tcatttatgg gcatactcaa cacccttcgg cacaatgcct tgaggatcca tagctaccct 840
gaaggatat gcctcagcca ggccagcaaa ctgggtctca tgagtctgca gagacctttc 900
cagatgagca ttgacatggg ctttaaaaca cgtgccttca cactatttt gattctcttt 960
gctgtcttca ttgtctgtg ggccccatto accacttaca gccttggtggc aacattcagt 1020
aagcactttt actatcagca caactttttt gagattagca cctggctact gtggctctgc 1080
tacctcaagt ctgcattgaa tccgctgac tactactgga ggattaagaa attccatgat 1140
gcttgcttg acatgatgcc taagtctt c aagttttgc cgcagctccc tggtcacaca 1200
aagcgacgga tacgtcctag tgctgtctat gtgtgtggg aacatcggac ggtggtgtga 1260

```

<210> 8
 <211> 419
 <212> PRT
 <213> Homo sapiens

<400> 8

```

Met Val Phe Ser Ala Val Leu Thr Ala Phe His Thr Gly Thr Ser Asn
  1             5             10             15

Thr Thr Phe Val Val Tyr Glu Asn Thr Tyr Met Asn Ile Thr Leu Pro
          20             25             30

Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe
          35             40             45

Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr
          50             55             60

Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu
          65             70             75             80

```


Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe
85 90 95

Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met
100 105 110

Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met
115 120 125

Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr
130 135 140

Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val Ser Ala Met Phe
145 150 155 160

Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser
165 170 175

Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro
180 185 190

Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys
195 200 205

Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser
210 215 220

Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln
225 230 235 240

Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu
245 250 255

Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn
260 265 270

Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala
275 280 285

Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile
290 295 300

Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe
305 310 315 320

Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val
325 330 335

Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile
 340 345 350

Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro
 355 360 365

Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp
 370 375 380

Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr
 385 390 395 400

Lys Arg Arg Ile Arg Pro Ser Ala Val Tyr Val Cys Gly Glu His Arg
 405 410 415

Thr Val Val

<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
 forward EDG-1

<400> 9

tcatcgtccg gcattacaac ta

22

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
 reverse EDG-1

<400> 10

gagtgaagctt gtaggtggtg

20

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
forward EDG-2

<400> 11

agatctgacc agccgactca c

21

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
reverse EDG-2

<400> 12

gttggccatc aagtaataaa ta

22

<210> 13

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
forward EDG-3

<400> 13

cttggtcac tgcagcttca tc

22

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
reverse EDG-3

<400> 14

tgctgatgca gaaggcaatg ta

22

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer,
forward EDG-4

<400> 15
ctgctcagcc gctcctatatt g

21

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer,
reverse EDG-4

<400> 16
aggagcaccc acaagtcatt ag

22

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer,
forward EDG-5

<400> 17
atgggcagct tgtactcgga g

21

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer,
reverse EDG-5

<400> 18
cagccagcag acgataaaga c 21

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer,
forward EDG-6

<400> 19
tgaacatcac gctgagtgac ct 22

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer,
reverse EDG-6

<400> 20
gatcatcagc accgtcttca gc 22

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer,
forward EDG-7

<400> 21
agcaacactg atactgtcga tg 22

<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
reverse EDG-7

<400> 22

gcacccctcat gattgacatg tg

22

<210> 23

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
forward EDG-8

<400> 23

atctgtgcgc tctatgcaag ga

22

<210> 24

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
reverse EDG-8

<400> 24

ggtgtagatg ataggattca gca

23

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer,
forward PSP24

<400> 25

ctgcatcatc gtgtaccaga g

21

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: primer,
reverse PSP24

<400> 26

acgaactcta tgcaggcctc gc

22